

Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using SW model

Run on: September 15, 2004, 21:34:03 ; search time 44 Seconds

(without alignments)
2359.216 Million cell updates/sec

Title: US-10-081-775-2

Perfect score: 1718

Sequence: MSSTIGHMESPHTTDVDP.....RKRVVRVFQSGQMGIRASE 329

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SPTRMBL25:*

1: SP_archea:*

2: SP_bacteria:*

3: SP_fungi:*

4: SP_human:*

5: SP_invertebrate:*

6: SP_mammal:*

7: SP_mhc:*

8: SP_organelle:*

9: SP_phage:*

10: SP_plant:*

11: SP_rhodopsin:*

12: SP_virus:*

13: SP_vertebrate:*

14: SP_unclassified:*

15: SP_virus:*

16: SP_bacteriophage:*

17: SP_archaea:*

17	883.5	51.4	317	11	Q8VGU9	mus	musculu
18	883	51.4	316	11	Q7TRR5	mus	musculu
19	883	51.4	327	11	Q8VFB28	mus	musculu
20	883	51.4	339	11	Q8WU90	mus	musculu
21	882.5	51.4	312	11	Q8VGW2	mus	musculu
22	881.5	51.3	317	11	Q8VH04	mus	musculu
23	880.5	51.3	312	11	Q7TRR6	mus	musculu
24	877.5	51.1	316	11	Q7TRQ8	mus	musculu
25	877	51.0	341	11	Q8VFB27	mus	musculu
26	875	50.9	314	11	Q7TRR0	mus	musculu
27	873.5	50.8	312	11	Q8VGX4	mus	musculu
28	873	50.8	317	11	Q8VGY7	mus	musculu
29	871.5	50.7	316	11	Q8VGZ4	mus	musculu
30	871	50.7	319	11	Q8VGV9	mus	musculu
31	871	50.7	324	11	Q7TRP9	mus	musculu
32	870	50.6	314	11	Q7TRR2	mus	musculu
33	868.5	50.6	312	11	Q8VF06	mus	musculu
34	868.5	50.6	319	11	Q8VGW0	mus	musculu
35	867.5	50.5	314	11	Q7TRR0	mus	musculu
36	866	50.4	314	11	Q9EGQ6	mus	musculu
37	865	50.3	316	11	Q8VH03	mus	musculu
38	865	50.3	320	11	Q8Vbv9	mus	musculu
39	864.5	50.3	312	11	Q7TRP3	mus	musculu
40	860.5	50.1	308	11	Q8VG84	mus	musculu
41	858	49.9	314	11	Q7TRR7	mus	musculu
42	854	49.7	314	11	Q8Vew8	mus	musculu
43	852	49.6	318	11	Q8VH00	mus	musculu
44	851.5	49.6	317	4	Q8NGK5	homo sapien	musculu
45	851	49.5	322	11	Q8VGW5	mus	musculu

ALIGNMENTS

RESULT 1

ID	Q8VGX9	PRELIMINARY;	PRT;	329 AA.
AC	Q8VGX9;			
DT	01-MAR-2002 (T-EMBL2;	20, Created)		
DT	01-MAR-2002 (T-EMBL2;	20, Last sequence update)		
DT	01-JUN-2003 (T-EMBL2;	24, Last annotation update)		
DE	Olfactory receptor MOR27-1.			
OS	Mus musculus (Mouse)			
OC	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
RN	NCBI_TAXID=10050;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RA	Zhang X., Firestein S.J.;			
RA	"The olfactory receptor gene superfamily of the mouse.";			
RA	PL. Neurosci. 0:0 (2002).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RA	Adams M.J.			
RL	Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.			
DR	EMBL; AY073012; C:integer to membrane; IEA.			
DR	GO; GO:0016021; C:integer to membrane; IEA.			
DR	GO; GO:004872; :receptor activity; IEA.			
DR	GO; GO:001584; P:rhodopsin-like receptor activity; IEA.			
DR	GO; GO:0007186; P:G-protein coupled receptor protein signalin. . . ; IEA.			
DR	InterPro; IPR000776; GPCR_Rhodopsin.			
PF	PF00001; 7tm_1; 1.			
PRINTS	PR00271; GPCR_RHODOPSIN.			
DR	PROSITE; PS00217; G-PROTEIN RECEP_F1_1;			
DR	PROSITE; PS50262; G-PROTEIN RECEP_F1_2;			
KW	Receptor.			
SQ	SEQUENCE 329 AA; 36285 MW; 7D23203F650861EF CRC64;			

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Score	Match Length	DB ID	Description
1	1534	89.3	329	Q8VGX9
2	1517	88.3	321	Q7tP84
3	977.5	56.9	315	Q8VGZ3
4	936.5	54.5	299	Q8NGK2
5	936	54.5	316	Q7TRN7
6	927	54.0	317	11 Q8VGX8
7	912.5	53.1	319	Q8VGP8
8	907.5	52.8	317	Q8VEK9
9	891.5	51.9	311	Q7TRR4
10	890	51.9	317	11 Q8VGV8
11	890.5	51.8	323	Q8VGZ2
12	890	51.8	314	11 Q8VGZ2
13	880	51.8	318	11 Q8VGA1
14	887.5	51.7	316	11 Q8VG79
15	887.5	51.7	318	11 Q8VGV3
16	887.5	51.7	326	11 Q3WWD9

Query Match 89.3%; Score 1534; DB 11; Length 329;
Best Local Similarity 88.1%; Pred. No. 8.8e-135; Mismatches 18; Indels 0; Gaps 0;

1 MSSTLGHNMESPHTDVSFFFLIGIPLQGFLWLSLPVCGLGTATIVGNITLWVVA 60

1 MSNTISQMESEPNHTDLDPSIFFLGIPISEQFMWLSPVCCLGTTATIVNITLIVVVA 60
 61 TEPVLIHKPVYLFQMLSTIDLAASVSTVPLLAIFWCAGHISASACLAHMFFHAFM 120
 61 TEPTLRRVYLFQMLSTIDLAASVSTVPLLAIFWCAGHISASACLAHMFFHAFM 120
 121 ESTVLLAMAEDRYVACIPLRYATLITPTLIAHIGVAAVYRGSLIIMLPCPFFIGLNFQ 180
 121 ESTVLLAMAEDRYVACIPLRYSTLIDTIIARIAGVAMNRGSLSLMLPCFLIGLSFQ 180
 181 SHVILHTYCEHMAVVKLACGDTTRPNRYVGTAAVIVGDLFCIGLSYALIAQAVRLSS 240
 181 SHVIPHTYCEHMAVVKLACGDTTRPNRYVGLTAAVIVGDLFCIGLSYALIAQAVRLSS 240
 241 HEARSKALGTGCSHVCVLLISTYPALESFPTRFGHYPVHILLLANYLPLLPAALNPV 300
 241 QEARSKALGTGCSHVCVLLISTYPALESFPTRFGHYPVHILLLANYLPLLPAALNPV 300
 301 VGYVKTKQIKRKRVYRVRVYFQSGQNGKIASE 329
 301 VGYVKTRERVAKTQFWGQSTRLTSK 329

RESULT 2						
RP8	PRELIMINARY;	PRT;	321 AA.			
Q7TRP8; Q7TRP8;						
01-OCT-2003 (TREMBLrel. 25, Created)						
01-OCT-2003 (TREMBLrel. 25, Last sequence update)						
01-OCT-2003 (TREMBLrel. 25, Last annotation update)						
Olfactory receptor GA_X6K02T2PB9J-7245486-7246451.						
GA_X6K02T2PB9J-7245486-7246451.						
Mus musculus (Mouse).						
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.						
NCBI_TaxID=10090;						
[1]						
SEQUENCE FROM N.A.						
Young J.M., Shykoff B.M., Lane R.P., Tonnes-Priddy L., Ross J.A., Walker M., Williams E.M., Axel R., Trask B.J., "Odorant receptor ESTs demonstrate olfactory expression of over 400 genes, extensive alternate splicing, and unequal expression levels.", Submitted (JUN-2003) to the EMBL/GenBank/DBU databases.						
[2]						
SEQUENCE FROM N.A.						
Sanders K., Submitted (JUN-2003) to the EMBL/GenBank/DBU databases.						
EMBL; AY317777; AAP7129.1; -.						
Receptor.						
RESEQUENCE 321 AA; 35422 MW; 7E5B78779DEC4D0F CRC64;						
SEQUENCE						
Query Match 88.3%; Score 1517; DB 11; Length 321;						
Exact Locality Similarity 99.4%; Pred. No. 3.3e-13;						
Matches 287; Conservative 16; Mismatches 18; Indels 0; Gaps 0;						
RESEQUENCE						
9 MESPHHTDVPDSYFFELIGPGLQFHFLWLSLPVCIGLTATIVGNNTILIVVYATEPVLHHP 68						
1 MESPHHTDVPDSYFFELIGPGLQFHFLWLSLPVCIGLTATIVGNNTILIVVYATEPVLHHP 60						
69 VYFLFLCMUSTIDLAASVSTVPKLIAIFWCGAGHTSASAACLAHMFFTHAFCMMEESTYLAM 128						
61 VYFLFLCMUSTIDLAASVSTVPKLIAIFWCGAGHTSASAACLTQMFFTHAFCMMEESTYLAM 120						
129 AFDRYVAICHPLRYATLTDTIAIHGVAAVRSILMLPQCPFFIGRLNPFCQSHVILHTY 188						
121 AFDRYVAICHPLRYSTLTDTIAIHGVAAVRSILMLPQCPFFIGRLNPFCQSHVILHTY 180						
189 CEHMAYVVKLACGDTRPNNVGLTAALLVGVDFLFCIGLSYALIAOVLRLSHEARSKAL 248						
181 CEHMAYVVKLACGDTRPNNVGLTAALLVGVDFLFCIGLSYALIAOVLRLSHEARSKAL 240						